Figure 1A

ClustalW DNA Sequence Alignment of *sasp-B* Amplicons
from 38 *Bacillus anthracis* Strains

	1 15	16 30	31 45	46 60	61 75	76 90
1 Bapast	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
2 Barec1	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
3 NMRI#67	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
4 NMRI#63	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
5 NMRI#62	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
6 NMRI#60	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
7 NMRI#1	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
8 NMRI#2	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
9 NMRI#4	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
10 NMRI#5	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
11 NMRI#6	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
12 NMRI#10	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
13 NMRI#11	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
14 NMRI#18	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
15 NMRI#19	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
16 NMRI#20	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
17 NMRI#22	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
18 NMRI#23	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
19 NMRI#24	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
20 NMRI#25	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
21 NMRI#26	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
22 NMRI#28	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
23 NMRI#32	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
24 NMRI#35	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
25 NMRI#36	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
26 NMRI#38	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
27 NMRI#39	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
28 NMRI#40	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
29 NMRI#41	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
30 NMRI#42	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
31 NMRI#43	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
32 NMRI#50	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
33 NMRI#52	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
34 NMRI#53	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
35 NMRI#54	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
36 NMRI#55	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
37 NMRI#56	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
38 NMRI#59	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA

Figure 1B

ClustalW DNA Sequence Alignment of *sasp-B* Amplicons
from 38 *Bacillus anthracis* Strains

	91 … 105	106 … 120	121 … 135	136 … 150	151 … 165	166 … 180
1 Bapast	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GCTAGCATTCAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA
2 Barec1	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GCTAGCATTCAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA
3 NMRI#67	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GCTAGCATTCAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA
4 NMRI#63	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GCTAGCATTCAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA
5 NMRI#62	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GCTAGCATTCAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA
6 NMRI#60	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GCTAGCATTCAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA
7 NMRI#1	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GCTAGCATTCAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA
8 NMRI#2	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GCTAGCATTCAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA
9 NMRI#4	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GCTAGCATTCAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA
10 NMRI#5	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GCTAGCATTCAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA
11 NMRI#6	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GCTAGCATTCAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA
12 NMRI#10	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GCTAGCATTCAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA
13 NMRI#11	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GCTAGCATTCAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA
14 NMRI#18	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GCTAGCATTCAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA
15 NMRI#19	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GCTAGCATTCAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA
16 NMRI#20	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GCTAGCATTCAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA
17 NMRI#22	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GCTAGCATTCAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA
18 NMRI#23	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GCTAGCATTCAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA
19 NMRI#24	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GCTAGCATTCAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA
20 NMRI#25	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GCTAGCATTCAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA
21 NMRI#26	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GCTAGCATTCAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA
22 NMRI#28	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GCTAGCATTCAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA
23 NMRI#32	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GCTAGCATTCAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA
24 NMRI#35	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GCTAGCATTCAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA
25 NMRI#36	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GCTAGCATTCAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA
26 NMRI#38	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GCTAGCATTCAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA
27 NMRI#39	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GCTAGCATTCAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA
28 NMRI#40	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GCTAGCATTCAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA
29 NMRI#41	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GCTAGCATTCAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA
30 NMRI#42	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GCTAGCATTCAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA
31 NMRI#43	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GCTAGCATTCAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA
32 NMRI#50	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GCTAGCATTCAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA
33 NMRI#52	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GCTAGCATTCAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA
34 NMRI#53	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GCTAGCATTCAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA
35 NMRI#54	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GCTAGCATTCAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA
36 NMRI#55	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GCTAGCATTCAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA
37 NMRI#56	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GCTAGCATTCAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA
38 NMRI#59	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GCT<u>AGCATT</u>CAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA
				insertion region		

Figure 1C

ClustalW DNA Sequence Alignment of *sasp-B* Amplicons from 38 *Bacillus anthracis* Strains

	181	195 196	210 211	225 226	240	
1 Bapast	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA		(SEQ ID NO: 13)
2 Barec1	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA		(SEQ ID NO: 14)
3 NMRI#67	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA		(SEQ ID NO: 15)
4 NMRI#63	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA		(SEQ ID NO: 16)
5 NMRI#62	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA		(SEQ ID NO: 17)
6 NMRI#60	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA		(SEQ ID NO: 18)
7 NMRI#1	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA		(SEQ ID NO: 19)
8 NMRI#2	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA		(SEQ ID NO: 20)
9 NMRI#4	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA		(SEQ ID NO: 21)
10 NMRI#5	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA		(SEQ ID NO: 22)
11 NMRI#6	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA		(SEQ ID NO: 23)
12 NMRI#10	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA		(SEQ ID NO: 24)
13 NMRI#11	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA		(SEQ ID NO: 25)
14 NMRI#18	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA		(SEQ ID NO: 26)
15 NMRI#19	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA		(SEQ ID NO: 27)
16 NMRI#20	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA		(SEQ ID NO: 28)
17 NMRI#22	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA		(SEQ ID NO: 29)
18 NMRI#23	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA		(SEQ ID NO: 30)
19 NMRI#24	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA		(SEQ ID NO: 31)
20 NMRI#25	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA		(SEQ ID NO: 32)
21 NMRI#26	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA		(SEQ ID NO: 33)
22 NMRI#28	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA		(SEQ ID NO: 34)
23 NMRI#32	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA		(SEQ ID NO: 35)
24 NMRI#35	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA		(SEQ ID NO: 36)
25 NMRI#36	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA		(SEQ ID NO: 37)
26 NMRI#38	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA		(SEQ ID NO: 38)
27 NMRI#39	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA		(SEQ ID NO: 39)
28 NMRI#40	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA		(SEQ ID NO: 40)
29 NMRI#41	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA		(SEQ ID NO: 41)
30 NMRI#42	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA		(SEQ ID NO: 42)
31 NMRI#43	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA		(SEQ ID NO: 43)
32 NMRI#50	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA		(SEQ ID NO: 44)
33 NMRI#52	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA		(SEQ ID NO: 45)
34 NMRI#53	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA		(SEQ ID NO: 46)
35 NMRI#54	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA		(SEQ ID NO: 47)
36 NMRI#55	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA		(SEQ ID NO: 47)
37 NMRI#56	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA		(SEQ ID NO: 49)
38 NMRI#59	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA		(SEQ ID NO: 50)

Figure 2A

Drawing ClustalW Global *sasp-B* DNA Sequence Alignment of *Bacillus anthracis*, *Bacillus thuringiensis* and *Bacillus cereus* Strains

	1 – 15	16 – 30	31 – 45	46 – 60	61 – 75	76 – 90
1 NMRI#15	AACAAGGCAACTTCT	GGCGCTAGCATTCAA	AGTACAAATGCTAGT	TATGGTACAGAGTTT	TCAACTGAAACAGAT	GTGCAAGCAGTAAAA
2 1B	AACAAGGCAACTTCT	GGCGCTAGCATTCAA	AGTACAAATGCTAGT	TATGGTACAGAGTTT	TCAACTGAAACAGAT	GTGCAAGCAGTAAAA
3 003	AACAAGGCAACTTCT	GGCGCTAGCATTCAA	AGTACAAATGCTAGT	TATGGTACAGAGTTT	TCAACTGAAACAGAT	GTGCAAGCAGTAAAA
4 III	AACAAGGCAACTTCT	GGCGCTAGCATTCAA	AGTACAAATGCTAGT	TATGGTACAGAGTTT	TCAACTGAAACAGAT	GTGCAAGCAGTAAAA
5 IV	AACAAGGCAACTTCT	GGCGCTAGCATTCAA	AGTACAAATGCTAGT	TATGGTACAGAGTTT	TCAACTGAAACAGAT	GTGCAAGCAGTAAAA
6 BtB	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGTACAAATGCTAGT	TATGGTACAGAGTTT	TCAACTGAAACAGAT	GTACAAGCAGTAAAA
7 BtY	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGTACAAATGCTAGT	TATGGTACAGAGTTT	TCAACTGAAACAGAT	GTACAAGCAGTAAAA
8 4A1	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGTACAAATGCTAGT	TATGGTACAGAGTTT	GCAACTGAAACAAAT	GTACAAGCAGTAAAA
9 BtV	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGTACAAATGCTAGT	TATGGTACAGAGTTT	GCAACTGAAACAAAT	GTACAAGCAGTAAAA
10 BtZ	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGTACAAATGCTAGT	TATGGTACAGAGTTT	GCAACTGAAACAAAT	GTACAAGCAGTAAAA
11 Bcer3	AACAAAGCAACTTCT	GGTGCTAGCATTCAA	AGTACAAATGCTAGT	TATGGTACAGAGTTT	TCAACTGAAACAGAT	GTACAAGCTGTAAAA
12 1B/A	AACAAAGCAACTTCT	GGTGCTAGCATTCAA	AGTACAAATGCTAGT	TATGGTACAGAGTTT	TCAACTGAAACAGAT	GTACAAGCTGTAAAA
13 Bcerpub	AACAAAGCAACTTCT	GGTGCTAGCATTCAA	AGTACAAATGCTAGT	TATGGTACAGAGTTT	TCAACTGAAACAGAT	GTACAAGCTGTAAAA
14 BtT	AACAAAGCAACTTCT	GGTGCTAGCATTCAA	AGTACAAATGCTAGT	TATGGTACAGAGTTT	TCAACTGAAACAGAT	GTACAAGCTGTAAAA
15 BtU	AACAAAGCAACTTCT	GGTGCTAGCATTCAA	AGTACAAATGCTAGT	TATGGTACAGAGTTT	TCAACTGAAACAGAT	GTACAAGCTGTAAAA
16 BtS	AACAAAGCAACTTCT	GGTGCTAGCATTCAA	AGTACAAATGCTAGT	TATGGTACAGAGTTT	TCAACTGAAACAGAT	GTACAAGCTGTAAAA
17 BtR	AACAAAGCAACTTCT	GGTGCTAGCATTCAA	AGTACAAATGCTAGT	TATGGTACAGAGTTT	TCAACTGAAACAGAT	GTACAAGCTGTAAAA
18 BtL	AACAAAGCAACTTCT	GGTGCTAGCATTCAA	AGTACAAATGCTAGT	TATGGTACAGAGTTT	TCAACTGAAACAGAT	GTACAAGCTGTAAAA
19 BtO	AACAAAGCAACTTCT	GGTGCTAGCATTCAA	AGTACAAATGCTAGT	TATGGTACAGAGTTT	TCAACTGAAACAGAT	GTACAAGCTGTAAAA
20 BtJ	AACAAAGCAACTTCT	GGTGCTAGCATTCAA	AGTACAAATGCTAGT	TATGGTACAGAGTTT	TCAACTGAAACAGAT	GTACAAGCTGTAAAA
21 4J2	AACAAAGCAACTTCT	GGTGCTAGCATTCAA	AGTACAAATGCTAGT	TATGGTACAGAGTTT	TCAACTGAAACAGAT	GTACAAGCTGTAAAA
22 BtG	AACAAAGCAACTTCT	GGTGCTAGCATTCAA	AGTACAAATGCTAGT	TATGGTACAGAGTTT	TCAACTGAAACAGAT	GTACAAGCTGTAAAA
23 BtI	AACAAAGCAACTTCT	GGTGCTAGCATTCAA	AGTACAAATGCTAGT	TATGGTACAGAGTTT	TCAACTGAAACAGAT	GTACAAGCTGTAAAA
24 Bcer2	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGTACAAATGCTAGT	TATGGTACAGAGTTT	TCAACTGAAACAGAT	GTACAAGCTGTAAAA
25 BtC	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGTACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
26 BtE2	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGTACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
27 BtE4	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGTACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
28 BtK	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGTACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
29 BtM	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGTACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
30 BtN	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGTACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
31 BtP	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGTACAAATGCTAGT	TATGGTACAGAATTT	GCTACTGAAACAAAT	GTACAAGCAGTAAAA
32 BtX	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGTACAAATGCTAGT	TATGGTACAGAATTT	GCTACTGAAACAAAT	GTACAAGCAGTAAAA
33 Bcer1	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGTACAAATGCTAGT	TATGGTACAGAATTT	GCTACTGAAACAAAT	GTACAAGCAGTAAAA
34 BtQ	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGTACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
35 BtW	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGTACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
36 Bc #57	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGTACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA
37 Ba #11	AACAAGGCAACTTCT	GGTGCTAGCATTCAA	AGCACAAATGCTAGT	TATGGTACAGAGTTT	GCGACTGAAACAAAT	GTACAAGCAGTAAAA

Figure 2B

Drawing ClustalW Global *sasp-B* DNA Sequence Alignment of *Bacillus anthracis*, *Bacillus thuringiensis* and *Bacillus cereus* Strains

	91	105 106	120 121	135 136	150 151	165 166 180
1 NMRI#15	CAAGCAAATGCACAA	TCAGAAGCAAAGAAA	GCACAAGCTTCTGGT	GCA------CAAAGT	GCAAACGCTAGTTAT	GGTACTGAATTTGCA
2 1B	CAAGCAAATGCACAA	TCAGAAGCAAAGAAA	GCACAAGCTTCTGGT	GCA------CAAAGT	GCAAACGCTAGTTAT	GGTACTGAATTTGCA
3 003	CAAGCAAATGCACAA	TCAGAAGCAAAGAAA	GCACAAGCTTCTGGT	GCA------CAAAGT	GCAAACGCTAGTTAT	GGTACTGAATTTGCA
4 III	CAAGCAAATGCACAA	TCAGAAGCAAAGAAA	GCACAAGCTTCTGGT	GCA------CAAAGT	GCAAACGCTAGTTAT	GGTACTGAATTTGCA
5 IV	CAAGCAAATGCACAA	TCAGAAGCAAAGAAA	GCACAAGCTTCTGGT	GCA------CAAAGT	GCAAACGCTAGTTAT	GGTACTGAATTTGCA
6 BtB	CAAGCAAACGCACAA	TCAGAAGCAAAGAAA	GCACAAGCTTCTGGT	GCA------CAAAGT	GCAAACGCTAGTTAT	GGTACTGAATTTGCA
7 BtY	CAAGCAAACGCACAA	TCAGAAGCAAAGAAA	GCACAAGCTTCTGGT	GCA------CAAAGT	GCAAACGCTAGTTAT	GGTACAGAATTTGCA
8 4A1	CAAGCAAACGCACAA	TCAGAAGCAAAGAAA	GCACAAGCTTCTGGT	GCA------CAAAGT	GCAAACGCTAGTTAT	GGTACAGAATTTGCA
9 BtV	CAAGCAAACGCACAA	TCAGAAGCAAAGAAA	GCACAAGCTTCTGGT	GCA------CAAAGT	GCAAACGCTAGTTAT	GGTACAGAATTTGCA
10 BtZ	CAAGCAAACGCACAA	TCAGAAGCAAAGAAA	GCACAAGCTTCTGGT	GCA------CAAAGT	GCAAACGCTAGTTAT	GGTACAGAATTTGCA
11 Bcer3	CAAGCAAACGCACAA	TCAGAAGCAAAAAAA	GCACAAGCTTCTGGT	GCA------CAAAGT	GCAAACGCTAGTTAT	GGTACAGAATTTGCA
12 1B/A	CAAGCAAACGCACAA	TCAGAAGCAAAGAAA	GCACAAGCTTCTGGT	GCA------CAAAGT	GCAAACGCTAGTTAT	GGTACAGAATTTGCA
13 Bcerpub	CAAGCAAACGCACAA	TCAGAAGCAAAGAAA	GCACAAGCTTCTGGT	GCA------CAAAGT	GCAAACGCTAGTTAT	GGTACAGAATTTGCA
14 BtT	CAAGCAAACGCACAA	TCAGAAGCAAAGAAA	GCACAAGCTTCTGGT	GCA------CAAAGT	GCAAACGCTAGTTAT	GGTACAGAATTTGCA
15 BtU	CAAGCAAACGCACAA	TCAGAAGCAAAGAAA	GCACAAGCTTCTGGT	GCA------CAAAGT	GCAAACGCTAGTTAT	GGTACAGAATTTGCA
16 BtS	CAAGCAAACGCACAA	TCAGAAGCAAAGAAA	GCACAAGCTTCTGGT	GCA------CAAAGT	GCAAACGCTAGTTAT	GGTACAGAATTTGCA
17 BtR	CAAGCAAACGCACAA	TCAGAAGCAAAGAAA	GCACAAGCTTCTGGT	GCA------CAAAGT	GCAAACGCTAGTTAT	GGTACAGAATTTGCA
18 BtL	CAAGCAAACGCACAA	TCAGAAGCAAAGAAA	GCACAAGCTTCTGGT	GCA------CAAAGT	GCAAACGCTAGTTAT	GGTACAGAATTTGCA
19 BtO	CAAGCAAACGCACAA	TCAGAAGCAAAGAAA	GCACAAGCTTCTGGT	GCA------CAAAGT	GCAAACGCTAGTTAT	GGTACAGAATTTGCA
20 BtJ	CAAGCAAACGCACAA	TCAGAAGCAAAGAAA	GCACAAGCTTCTGGT	GCA------CAAAGT	GCAAACGCTAGTTAT	GGTACAGAATTTGCA
21 4J2	CAAGCAAACGCACAA	TCAGAAGCAAAGAAA	GCACAAGCTTCTGGT	GCA------CAAAGT	GCAAACGCTAGTTAT	GGTACAGAATTTGCA
22 BtG	CAAGCAAACGCACAA	TCAGAAGCAAAGAAA	GCACAAGCTTCTGGT	GCA------CAAAGT	GCAAACGCTAGTTAT	GGTACAGAATTTGCA
23 BtI	CAAGCAAACGCACAA	TCAGAAGCAAAGAAA	GCACAAGCTTCTGGT	GCA------CAAAGT	GCAAACGCTAGTTAT	GGTACAGAATTTGCA
24 Bcer2	CAAGCAAACGCACAA	TCAGAAGCAAAGAAA	GCACAAGCTTCTGGT	GCA------CAAAGT	GCAAACGCTAGTTAT	GGTACAGAATTTGCA
25 BtC	CAAGCAAACGCACAA	TCAGAAGCAAAGAAA	GCACAAGCTTCTGGT	GCA------CAAAGT	GCAAACGCTAGTTAT	GGTACAGAATTTGCA
26 BtE2	CAAGCAAACGCACAA	TCAGAAGCAAAGAAA	GCACAAGCTTCTGGT	GCA------CAAAGT	GCAAACGCTAGTTAT	GGTACAGAATTTGCA
27 BtE4	CAAGCAAACGCACAA	TCAGAAGCAAAGAAA	GCACAAGCTTCTGGT	GCA------CAAAGT	GCAAACGCTAGTTAT	GGTACAGAATTTGCA
28 BtK	CAAGCAAACGCACAA	TCAGAAGCAAAGAAA	GCACAAGCTTCTGGT	GCA------CAAAGT	GCAAACGCTAGTTAT	GGTACAGAATTTGCA
29 BtM	CAAGCAAACGCACAA	TCAGAAGCAAAGAAA	GCACAAGCTTCTGGT	GCA------CAAAGT	GCAAACGCTAGTTAT	GGTACAGAATTTGCA
30 BtN	CAAGCAAACGCACAA	TCAGAAGCAAAGAAA	GCACAAGCTTCTGGT	GCA------CAAAGT	GCAAACGCTAGTTAT	GGTACAGAATTTGCA
31 BtP	CAAGCAAACGCACAA	TCAGAAGCAAAGAAA	GCACAAGCTTCTGGT	GCA------CAAAGT	GCAAACGCTAGTTAT	GGTACAGAATTTGCA
32 BtX	CAAGCAAACGCACAA	TCAGAAGCAAAGAAA	GCACAAGCTTCTGGT	GCA------CAAAGT	GCAAACGCTAGTTAT	GGTACAGAATTTGCA
33 Bcer1	CAAGCAAACGCACAA	TCAGAAGCAAAGAAA	GCACAAGCTTCTGGT	GCA------CAAAGT	GCAAACGCTAGTTAT	GGTACAGAATTTGCA
34 BtQ	CAAGCAAACGCACAA	TCAGAAGCAAAGAAA	GCACAAGCTTCTGGT	GCA------CAAAGT	GCAAACGCTAGTTAT	GGTACAGAATTTGCA
35 BtW	CAAGCAAACGCACAA	TCAGAAGCAAAGAAA	GCACAAGCTTCTGGT	GCA------CAAAGT	GCAAACGCTAGTTAT	GGTACAGAATTTGCA
36 NMRI#57	CAAGCAAACGCACAA	TCAGAAGCAAAGAAA	GCACAAGCTTCTGGT	GCA------CAAAGT	GCAAACGCTAGCTAT	GGTACAGAATTTGCA
37 NMRI#11	CAAGCAAACGCACAA	TCAGAAGCTAAGAAA	GCGCAAGCTTCTGGT	GC**TAGCATT**CAAAGC	ACAAATGCTAGTTAT	GGTACAGAATTTGCA

Figure 2C

Drawing ClustalW Global *sasp-B* DNA Sequence Alignment of *Bacillus anthracis, Bacillus thuringiensis* and *Bacillus cereus* Strains

	181	195 196	210 211	225 226	240
1 NMRI#15	ACTGAAACAGATGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA	(SEQ ID NO: 51)
2 1B	ACTGAAACAGATGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA	(SEQ ID NO: 52)
3 003	ACTGAAACAGATGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA	(SEQ ID NO: 53)
4 III	ACTGAAACAGATGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA	(SEQ ID NO: 54)
5 IV	ACTGAAACAGATGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA	(SEQ ID NO: 55)
6 BtB	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA	(SEQ ID NO: 56)
7 BtY	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA	(SEQ ID NO: 57)
8 4A1	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCTAAGTCA	GCTGCAAAACAA	(SEQ ID NO: 58)
9 BtV	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCTAAGTCA	GCTGCAAAACAA	(SEQ ID NO: 59)
10 BtZ	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCTAAGTCA	GCTGCAAAACAA	(SEQ ID NO: 60)
11 Bcer3	ACTGAAACAGACGTG	CATTCTGTGAAAAAA	CAAAATGCTAAGTCA	GCTGCAAAACAA	(SEQ ID NO: 61)
12 1B/A	ACTGAAACAGACGTG	CATTCTGTGAAAAAA	CAAAATGCTAAGTCA	GCTGCAAAACAA	(SEQ ID NO: 62)
13 Bcerpub	ACTGAAACAGACGTG	CATTCTGTGAAAAAA	CAAAATGCTAAGTCA	GCTGCAAAACAA	(SEQ ID NO: 63)
14 BtT	ACTGAAACAGACGTG	CATTCTGTGAAAAAA	CAAAATGCTAAGTCA	GCTGCAAAACAA	(SEQ ID NO: 64)
15 BtU	ACTGAAACAGACGTG	CATTCTGTGAAAAAA	CAAAATGCTAAGTCA	GCTGCAAAACAA	(SEQ ID NO: 65)
16 BtS	ACTGAAACAGACGTG	CATTCTGTGAAAAAA	CAAAATGCTAAGTCA	GCTGCAAAACAA	(SEQ ID NO: 66)
17 BtR	ACTGAAACAGACGTG	CATTCTGTGAAAAAA	CAAAATGCTAAGTCA	GCTGCAAAACAA	(SEQ ID NO: 67)
18 BtL	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCTAAGTCA	GCTGCAAAACAA	(SEQ ID NO: 68)
19 BtO	ACTGAAACAGACGTG	CATTCTGTGAAAAAA	CAAAATGCTAAGTCA	GCTGCAAAACAA	(SEQ ID NO: 69)
20 BtJ	ACTGAAACAGACGTG	CATTCTGTGAAAAAA	CAAAATGCTAAGTCA	GCTGCAAAACAA	(SEQ ID NO: 70)
21 4J2	ACTGAAACAGACGTG	CATTCTGTGAAAAAA	CAAAATGCTAAGTCA	GCTGCAAAACAA	(SEQ ID NO: 71)
22 BtG	ACTGAAACAGACGTG	CATTCTGTGAAAAAA	CAAAATGCTAAGTCA	GCTGCAAAACAA	(SEQ ID NO: 72)
23 BtI	ACTGAAACAGACGTG	CATTCTGTGAAAAAA	CAAAATGCTAAGTCA	GCTGCAAAACAA	(SEQ ID NO: 73)
24 Bcer2	ACTGAAACAGACGTG	CATTCTGTGAAAAAA	CAAAATGCTAAGTCA	GCTGCAAAACAA	(SEQ ID NO: 74)
25 BtC	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCTAAGTCA	GCTGCAAAACAA	(SEQ ID NO: 75)
26 BtE2	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCTAAGTCA	GCTGCAAAACAA	(SEQ ID NO: 76)
27 BtE4	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCTAAGTCA	GCTGCAAAACAA	(SEQ ID NO: 77)
28 BtK	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCTAAGTCA	GCTGCAAAACAA	(SEQ ID NO: 78)
29 BtM	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCTAAGTCA	GCTGCAAAACAA	(SEQ ID NO: 79)
30 BtN	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCTAAGTCA	GCTGCAAAACAA	(SEQ ID NO: 80)
31 BtP	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCTAAGTCA	GCTGCAAAACAA	(SEQ ID NO: 81)
32 BtX	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCTAAGTCA	GCTGCAAAACAA	(SEQ ID NO: 82)
33 Bcer1	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCTAAGTCA	GCTGCAAAACAA	(SEQ ID NO: 83)
34 BtQ	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCTAAGTCA	GCTGCAAAACAA	(SEQ ID NO: 84)
35 BtW	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCTAAGTCA	GCTGCAAAACAA	(SEQ ID NO: 85)
36 NMRI#57	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCTAAGTCA	GCTGCAAAACAA	(SEQ ID NO: 86)
37 NMRI#11	ACTGAAACAGACGTG	CATGCTGTGAAAAAA	CAAAATGCACAATCA	GCTGCAAAACAA	(SEQ ID NO: 87)

Figure 3 *Bacillus globigii* specific PCR targeting Bg sasp-gamma

Alignment of B. subtilis sasp-gamma sequence (from GeneBank) with B. globigii sequence (upper strand) showing the location of the primer sequences and how their sequence compares to the (known) B. subtilis sequence:

```
                 1             15 16            30 31            45 46            60 61            75 76             90
BgSSPE_edited_   --------------- --------------- --------------- --------------- ---------ATTCTA ATTGTCGTGGAGGTG
Bs_pub_SSPE      TTGACGCGGACGCTC ACTGCTCGTTTAAAA ATTTTTAAAAAAGAG GAATAGCTATACGAT CACCTGCACATTCTA ATGAGCGTGGAGGTG

                    Forward primer (BgSaspGam5')

                 91           105 106           120 121           135 136           150 151           165 166           180
BgSSPE_edited_   ATAAGATGGCTAAC  TCAAACAAC------ AAAACAAACGCTCAA CAAGTAAGAAAACAA AACCAACAATCAGCA TCTGGCCAAGGTCAG
Bs_pub_SSPE      ATAACAATGGCTAAC TCAAATAACTTCAGC AAAACAAACGCTCAA CAAGTTAGAAAACAA AACCAACAATCAGCT GCTGGTCAAGGTCAA

                                                  <-- Reverse primer (BgSaspGam3')

                 181           195 196           210 211           225 226           240 241           255 256           270
BgSSPE_edited_   TTTGGTACAGAATTT GCTAGCGAAACAAAC GTACAACAAGTAAGA AAACAAAACCAACAA TCAGCTGCTGGACAA GGACAATTCGGCACT
Bs_pub_SSPE      TTTGGCACTGAATTT GCTAGCGAAACAAAC GGTCAGCAAGTCAGA AAACAAAACCAGCAA TCAGCTGGACAACAA GGTCAATTCGGCACT

                 271           285 286           300 301           315 316           330 331           345 346           360
BgSSPE_edited_   GAATTCGCTAGTGAA ACTGATGCTCAGCAA GTAAGACAGCAAAAC CAATCTGCTGAACAA AACAAACAACAAAAC AGCTAATCACTGAAA
Bs_pub_SSPE      GAATTCGCTAGTGAA ACTGACGCACAGCAG GTAAGACAGCAAAAC CAATCTGCTGAACAA AACAAACAACAAAAC AGCTAATCACTGAAA

                 361           375 376           390 391           405 406           420 421           435 436           450
BgSSPE_edited_   CAGAAAAAAAGCACT TCATCCTCGGGTGGA AGTGCTTTTTTCTTT TTATAAAACGACAAA ACTTGTGGAA         355
Bs_pub_SSPE      CAGAAAAAA-GCACT TCATCTTCGG----- --------------- --------------- ----------         384
```

BgSSPE_edited (SEQ ID NO 110)
Bs_pub_SSPE (SEQ ID NO 111)